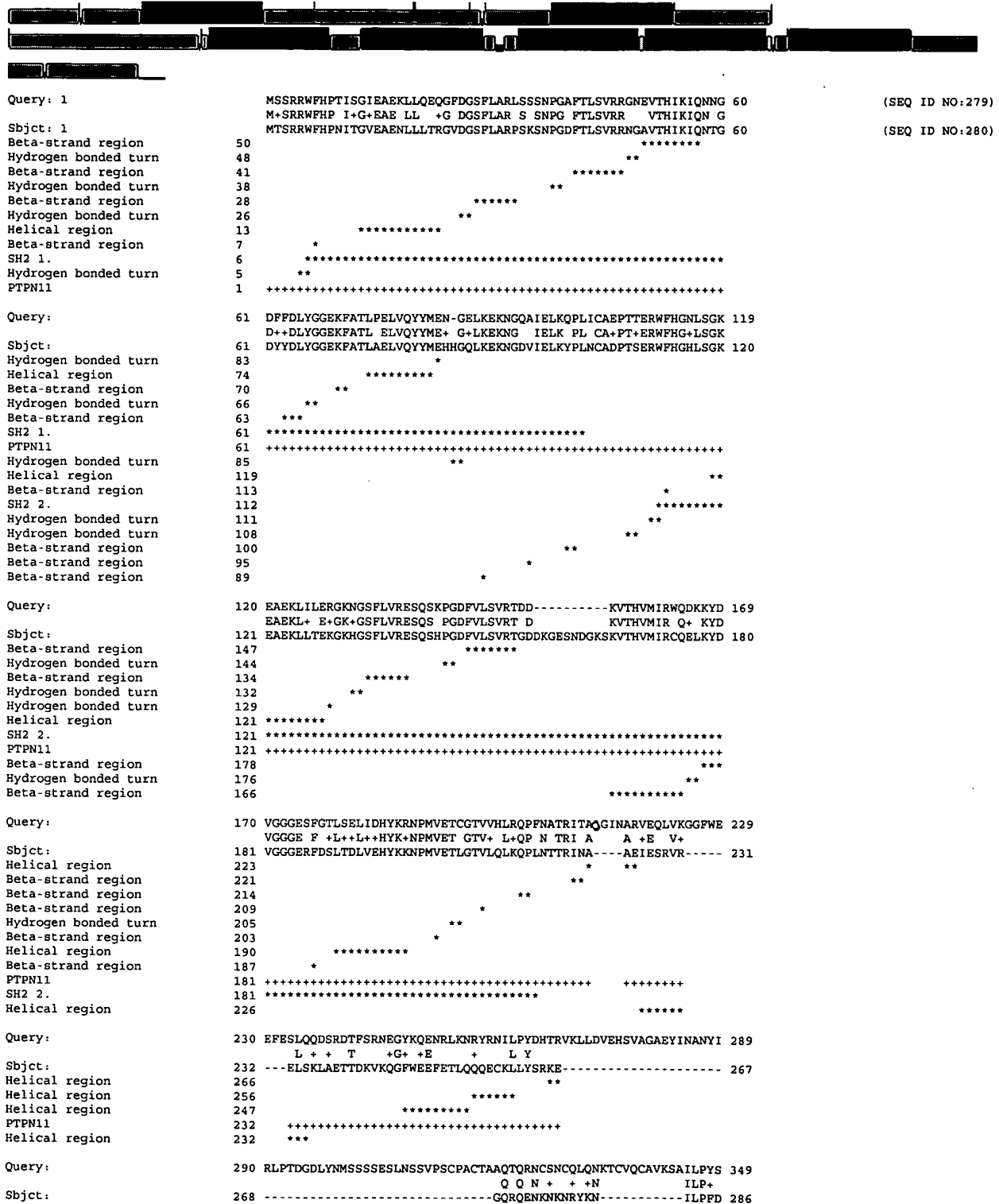


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FIGURE 2

Score = 553 bits (1425), Expect = e-156
Identities = 327/700 (46%), Positives = 406/700 (57%), Gaps = 152/700 (21%)



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```
Hydrogen bonded turn      280
PROTEIN-TYROSINE PHOSPHATASE. 276
Helical region            271
PTPN11                    268
Helical region            268
Hydrogen bonded turn      286

Query:                    350 NCATCSRKSDSLSKHKRSESSASSPSSGSGSGPGSSGTSVSSVNGPGTPTNLTSGTAG 409
+ D P P +
Sbjct:                    287 HTRVVLHDGD-----PNEPVS----- 302
Beta-strand region        289 ***
Hydrogen bonded turn      287 **
PTPN11                    287 ++++++++
PROTEIN-TYROSINE PHOSPHATASE. 287 *****

Query:                    410 CLVGLLKRHSNDSSGAVSISMAERERE-REREMFKTYIATQGCLLTQQVNTVTDFWNMVW 468
D A + I M E E + + K+YIATQGCL NTV DFW MV+
Sbjct:                    303 -----DYINA-NIIMPEFETKCNNSKPKKSYIATQGCLQ---NTVNDPWRMV 346
Beta-strand region        304 *****
PTPN11                    303 ++++++
PROTEIN-TYROSINE PHOSPHATASE. 303 *****
Hydrogen bonded turn      335 *
Beta-strand region        327 ****
Helical region            338 *****

Query:                    469 QENRVIIVMTTKEYERGKEKCARYWPDEGRSEQFGHARIQCVSENSTSDYTLREFLVSWR 528
QEN+RVIIVMTTKE ERGK KC +YWPDE ++G R++ V E++ DYTLRE +S
Sbjct:                    347 QENSRVIIVMTTKEYERGKSKCVKYWPDEYALKEYGVMVRNVKESAAHDYTLRELKLSKV 406
Hydrogen bonded turn      406 *
Beta-strand region        396 *****
Beta-strand region        383 *****
Hydrogen bonded turn      381 **
Beta-strand region        377 ****
Hydrogen bonded turn      374 **
Beta-strand region        364 **
Hydrogen bonded turn      362 **
Beta-strand region        360 **
Beta-strand region        352 ****
Hydrogen bonded turn      349 *
Helical region            347 **
PTPN11                    347 ++++++++
PROTEIN-TYROSINE PHOSPHATASE. 347 *****

Query:                    529 DQ--PARRIFHYHFQVWPDHGVDPADPGCVLNFQDVNTRQSHLAQAGEKPGPICVHCSAG 586
Q R ++ YHF+ WPDHGVDP+DPG VL+FL++V+ +Q + AG P+ VHCSAG
Sbjct:                    407 GQGNTERTVWQYHFRTPDHDGVPSDPGGVLDPLEEVHKKQESIMDAG---PVVVHCSAG 462
Beta-strand region        408 *****
Hydrogen bonded turn      407 *
PTPN11                    407 ++++++++
PROTEIN-TYROSINE PHOSPHATASE. 407 *****
Hydrogen bonded turn      450 **
Helical region            432 *****
active                    459 *
Beta-strand region        455 ****

Query:                    587 IGRTGTFIVIDMILDQIVRNLDTDEIDQRTIQMVRSGVQTEAQYKFVYVAVQHYI 646
IGRTGTFIVID++D I G+D +ID+ +TIQMVRSGVQTEAQY+F+Y AVQHYI
Sbjct:                    463 IGRTGTFIVIDILIDIIREKGVDCDIDVPKTIQMVRSGVMVQTEAQYRFIYMAVQHYI 522
Helical region            508 *****
Hydrogen bonded turn      502 **
Hydrogen bonded turn      499 **
Helical region            490 *****
Beta-strand region        487 **
Hydrogen bonded turn      484 **
Helical region            464 *****
PTPN11                    463 ++++++++
PROTEIN-TYROSINE PHOSPHATASE. 463 *****

Query:                    647 QTLIARKRAEEQSLQVGREYTNIKYTGEGNDSQRSPLPP 686
+TL R E++S + G EYTNIKY+ +SPLPP
Sbjct:                    523 ETLQRRIEEEQSKRKRGHEYTNIKYSLADQTSQDQSPPLPP 562
Conflict                    548 *
phosphorylation            542 *
Conflict                    535 *
Hydrogen bonded turn      524 *
Helical region            523 *
PTPN11                    523 ++++++++
```

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FIGURE 6A

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 1

BLAST P sequence alignment

Score = 616 bits (1588), Expect = e-175

Identities = 306/517 (59%), Positives = 390/517 (75%), Gaps = 24/517 (4%)



```

Query: 453 QPGSRYASTNVLAAPPGTPRAVST-----EDITREPTITIQKGPQGLGFNIVGGE 504      (SEQ ID NO:281)
          QP  + S +      P +P S      ++ITREPR + + +G GLGFNIVGGE
Sbjct: 425 QPVDNHVSPSSFLGQTPASPARYSPVSKAVLGDDEITREPRKVVLRHGSTGLGFNIVGGE 484      (SEQ ID NO:282)

Query: 505 DGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTLAQ 564
          DG+GI++SFILAGGPADL EL++GD+++SVN+V+L A+HE+AA ALK +G VT++AQ
Sbjct: 485 DGEGIFISFILAGGPADLSGELKGDRIISVNSVDLRAASHEQAAAAALKNAGQAVTIVAQ 544

Query: 565 YRPEEYNRFEARIQELKQXXXXXXXXXXXXXX-XXQKRSLYVRALFDYDPNRDDGLPSRG 623
          YRPEEY+RFEA+I +L++Q      QKRSLYVRALFDYD +D GLPS+G
Sbjct: 545 YRPEEYSRFEAKIHDRLREQMNSSISSGSGSLRTSQKRSLYVRALFDYDKTKDSGLPSQG 604

Query: 624 LPFKHGDILHVTNASDDEWQARRVLGDNEDEQIGIVPSKRRWERKMRARDRSVKFQGH 683
          L FK GDILHV NASDDEWQAR+V D E +++G++PSKRR E+K RAR ++VKF
Sbjct: 605 LNFKFDILHVINASDDEWQARQVTPDGESDEVGVIPSKRRVEKKERARLKTVKFN--- 661

Query: 684 AANNLNDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDGSDQEPNGVVSSTSEIDIXXXXX 743
          + DK + + K+K FSRKFPP K++D+ ++ SD + + V S+ S+ +
Sbjct: 662 --SKTRDKQSFNDKRRKNLFSRKFPFYKNKDQSEQETSDADQH-VTSNASDSE----- 712


Query: 744 XXXXXXXXXXXXXVLSYEAQRLSINYTRPVIILGPLKDRINDDLISEYDPDKFGSCVPHTT 803
          VLSYE V + +NYTRPVIILGP+KDRINDDLISE+PDKFGSCVPHTT
Sbjct: 713 ---SSYRQEYVLSYEPVNVQEVNYTRPVIILGPMKDRINDDLISEFPDKFGSCVPHTT 769

Query: 804 RPKREYEVDGRDYHFVSSREQMERDIQNHLFIEAGQYNDNLYGTSVASVREVAEKGHCI 863
          RPKR+YEVDGRDYHFV+SREQME+DIQ H FIEAGQYN++LYGTSV SVREVA KGKHCI
Sbjct: 770 RPKRDYEVDGRDYHFVTSREQMEKDIQEHKFIEAGQYNNHLYGTSVQSVREVAGKGKHCI 829

Query: 864 LDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRMTTEEAKKTYERAIMEQEFGY 923
          LDVSGNAIKRLQ+AQLYP+++FIKPKS+++MEMN+R+TEEA+KT+ERA+K+EQEF E+
Sbjct: 830 LDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNKRLTEEQARKTFERAMKLEQEFT 889

Query: 924 FTGVVQGDITIEEYISKVKSMIWSQSGPTIWVPSKESL 960
          FT +VQGDT+E+IY++VK +I QSG IWVP+KE L
Sbjct: 890 FTAIVQGDITLEDIYNQVKQIEEQSGSYIWVPAKEKL 926
Score = 206 bits (524), Expect = 2e-51
Identities = 119/227 (52%), Positives = 146/227 (63%), Gaps = 30/227 (13%)

```



```

Query: 24 LFNLDS-----VNGDDS-WLYEDIQLERGNGLGFSIAGGTDNPHIGTDTSIYITKLIS 76      (SEQ ID NO:283)
          L N DS      VNG D+ + YE+I LERGNGLGFSIAGGTDNPHIG D+SI+ITK+I+
Sbjct: 201 LVNTDSLETPTYVNGTDADYEYEEITLERGNGLGFSIAGGTDNPHIGDSSIFITKIIT 260      (SEQ ID NO:284)

Query: 77 GGAAAADGRLXXXXXXXXXXXXXXXXXPHASAVDALKKAGNVVKLHVKRKXXXXXXXXXXXX 136
          GGAAA DGRL      H+ AV+ALK+AG++V+L+VKR+
Sbjct: 261 GGAAAQDGRRLRVNDCILQVNEVDVRDVTSHKAVEALKEAGSIVRLYVKKRKPVS----- 315
Query: 137 XXXXXXXXXXXXXXXXVIEIDLKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQV 196

```

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Sbjct: 316 -----K++EI L+KG KGLGFSIAGG+GNQHIPGDN IYVTK+ +GG A
KIMEIKLIKPGKGLGFSIAGGVGNQHIPGDN SIYVTKIIEGGAHK 361

Query: 197 DGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLLIGK 243

DG+L IGDKL+AV + LE VTHE AV LK+ +D V L + K

Sbjct: 362 DGKLQIGDKLLAV---NNVCLEEVTHEEAVTALKNTSDFVYLKVAK 404

Score = 88.2 bits (217), Expect = 7e-16

Identities = 68/234 (29%), Positives = 95/234 (40%), Gaps = 43/234 (18%)



Query: 40 DIQLERGNISGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLXXXXXXXXXXXXX 99

(SEQ ID NO:285)

+I+L +G GLGFSIAGG N HI D SIY+TK+I GGAA DG+L

Sbjct: 319 EIKLIKPGKGLGFSIAGGVGNQHIPGDN SIYVTKIIEGGAHKDGKLQIGDKLLAVNNVC 378

(SEQ ID NO:286)

Query: 100 XXXXPHASAVDALKKAGNVVKLHVKKXXXXXXXXXXXXXXXXXXXXXKVI----- 153

H AV ALK + V L V + V

Sbjct: 379 LEEVTHEEAVTALKNTSDFVYLKVAKPTSMYMNDGYAPPDITNSSSQPVDNHVSPSSFLG 438

Query: 154 -----EIDLKVGKGLGFSIAGGIGNQHIPGDNGIYVT 186

++ L +G GLGF+I GG + GI+++

Sbjct: 439 QTPASPARYSPVSKAVLGDEITREPRKVVLRGSTGLGFNIVGGEDGE-----GIFIS 492

Query: 187 KLTGGRAGQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLLI 240

+ GG A + G L GD++I+V + +L +HE A A LK+ VT++

Sbjct: 493 FILAGGPADLSGELRKGDRIISV---NSVDLRAASHEQAAAALKNAGQAVTIV 542

Score = 70.1 bits (170), Expect = 2e-10

Identities = 47/141 (33%), Positives = 69/141 (48%), Gaps = 12/141 (8%)



Query: 432 MPALPVESNQTNRSQSPQPRQPGSRYASTNVLAAPVPGTPRAVSTEDITREPTITIQL 491

(SEQ ID NO:287)

+P LPV + T PQ P +T+ L TP V+ D E IT+++

Sbjct: 176 IPVLPVPAENTVILPTIPQANPPPV-LVNTDSLE-----TPTYVNGTDADYEYEEITLER 229

(SEQ ID NO:288)

Query: 492 GPQGLGFNIVGGEDG-----QGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATH 545

G GLGF+I GG D I+++ I+ GG A L+ D +L VN V++ TH

Sbjct: 230 GNSGLGFSIAGGTDNPHIGDDSSIFITKIITGGAAQDGRRLVNDICILQVNEVDVRDVTH 289

Query: 546 EEAAQALKTSGGVVTLAQYR 566

+A +ALK +G +V L + R

Sbjct: 290 SKAVEALKEAGSIVRLYVKRR 310

Score = 67.4 bits (163), Expect = 1e-09

Identities = 39/81 (48%), Positives = 49/81 (60%), Gaps = 6/81 (7%)



Query: 487 ITIQKGPQGLGFNIVGGEDGQ-----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNL 540

(SEQ ID NO:289)

I + KGP+GLGF+I GG Q IYV+ I+ GG A +L+ GD+LL+VNNV L

Sbjct: 320 IKLIKPGKGLGFSIAGGVGNQHIPGDN SIYVTKIIEGGAHKDGKLQIGDKLLAVNNVCL 379

(SEQ ID NO:290)

Query: 541 THATHEEAAQALKTSGGVVTL 561

THEEA ALK + V L

Sbjct: 380 EEVTHEEAVTALKNTSDFVYL 400

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FIGURE 6B

CLUSTAL W (1.82) sequence alignment

Drosophila	MTTRKKKRDGGGSGGGFIKKVSSLFNLDVNGDDSWLYEDIQLERGNISGLGFSIAGGTDN	60	(SEQ ID NO:291)
Human	MPVRKQD-----TQRALHLLLEEYRSKLSQTEDRQLRSSIERVINIFQSNLFQ	47	(SEQ ID NO:267)
	*..**:. . . : * . . . ** * . . . : . . . :		
Drosophila	PHIGTDTSIYITKLISGGAADGRLSINDIIVSVNDVSVVDVPHASAVDALKKAGNVVK	120	
Human	ALIDIQEFYEVTLTDN--PKCID-RSKPSEPIQPVNTWEISSLPSTVTSETLPSSLSPS	104	
	. * . : : * * . . . * . . : * . * . : . : * : . . . : . . . :		
Drosophila	LHVKRKRGTATTPAAGSAAGDARDSAASGPKVIEIDLKVGKGLGFSIAGGIGNQHHPGD	180	
Human	VEKYRQDEDTTPQEHISP--QITNEVIGPELVHVSEKN--LSEIENVHGFVSHSHIS-P	159	
	: . * : . * . * : . . . * : : : . : . . : * : : : * . :		
Drosophila	NGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNGSEKN---LENVTHELAVATLKSITDKV	237	
Human	IKPTEAVLPSPPTVPVIVLPVPAENTVILPTIPQANPPPVLVNTDSLETPTYVNGTDAD	219	
	: * . . . * * . : : . : . . : * : : * . * . * . * . *		
Drosophila	TLIIGKTQHLTTSAS---GGGGGGLSSGQQLSQSQSLATSQSQSQVHQQHATPMVNS	293	
Human	YEYEEITLERGNISGLGFSIAGGTDNPHIGDDSSIFITKIIITGGAAQDGRLRVNDICILQV	279	
	* . . * . . * . * . * : : * : : : * . : : * : : : : :		
Drosophila	QSTGALNSMGQTVVDSPSIPQAAAAVAAAANASASASVIASNNNTISNTTVTVTATATAS	353	
Human	NEVDVRDVTHSKAVEALKEAGSIVRLYVKKRKPVSEKIMEIK-LIKGPKGLGFSIAGGVG	338	
	: . . . : . . * : : . . : * : : : * . . . : . : . .		
Drosophila	NDSSKLPPSLGANSSISISNSNSNSNSNNINNINSINNNSSSSSTTATVAAATPTAASA	413	
Human	NQHHPGDNSIYVTKIIEGGAHKGDKLQIGDKLLAVNNVCLEEVTHEEAVTALKNTSDFV	398	
	* : * : . . * . . : : : : : : : : : : * . . : : * : * . * : .		
Drosophila	AAAAASSPPANSFYNNASMPALPVESNQTNRSQSPQPRQPGSRYASTNVLAAVPPGTPR	473	
Human	YLKVAK-PTSMYMNDGYAPPDITNSSSQPVDNHVSPSS-FLGQTPASP---ARYSPVSKA	453	
	. * . * : : : : * : . * . * . . * . . * . * . * . * . *		
Drosophila	AVSTEDITREPRITITIQKGPQGLGFNIVGGEDGQGIYVSFILAGGPADLGSELKRGDQLL	533	
Human	VLGDDEITREPRKVVLRHGSTGLGFNIVGGEDGEGIFISFILAGGPADLSGELKRGDRII	513	
	: . . : : * : : : : * . * : : : : : : : : : : : : : : : : : :		
Drosophila	SVNNVNLTHATHEEAAQALKTSGGVVTLAQYRPEEYNRFEARIQELKQQAALGAGGSGT	593	
Human	SVNSVDLRAASHEQAAAALKNAGQAVTIVAQYRPEEYSRFEAKIHDLRQMNSSISSGS	573	
	* * . * : * : * : * : * : * : * : * : * : * : * : * : * : * :		
Drosophila	-LLRTTQKRSLYVRALFDYDPNRDDGLPSRGLPFKHGDIHVTNASDDEWWQARRVLGDN	652	
Human	GSLRTSQKRSLYVRALFDYDKTKDGLPSQGLNFKFGDILHVINASDDEWWQARQVTPDG	633	
	* * : * : * : * : * : * : * : * : * : * : * : * : * : * : *		
Drosophila	EDEQIGIVPSKRRWERKMRARDRSVKFQGHAAANNLDKQSTLDRKKKNFTFSRKFPFMK	712	
Human	ESDEVGVIPSKRRVEKKERARLTKVKFN---SKTRDKGQSFNDKRKNLFSRKFPFYK	688	
	* . : : : : * : * : * : * : * : * : * : * : * : * : * : * : *		
Drosophila	SRDEKNEDGSDQEPNGVVSSTSEIDINNVMNNQSNPQPSEENVLSYEAVQRLSINYTRP	772	
Human	NKDQSEQETSDADQH-VTSNADSESSYRQG-----EEYVLSYEPVNVQEVNYTRP	738	
	: * : : : : * : : : * . * : : : . . : * * * * . * : : : * * * *		
Drosophila	VIIIGPLKDRINDDLISEYDPKFGSCVPHTTRPKREYVDGRDYHFVSSREQMERDIQNH	832	
Human	VIIIGPMKDRINDDLISEFPDKFGSCVPHTTRPKRDYVDGRDYHFVTSREQMEKDIQEH	798	
	* * * * : * * * * * : * * * * * : * * * * * : * * * * : * * : *		

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Drosophila LFI EAGQYNDNLYGTSVASVREVAEKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVD 892
Human KFI EAGQYNHLYGTSVQSVREVAGKGKHCILDVSGNAIKRLQIAQLYPISFIKPKSME 858
*****:***** ***** *****:*****::*****:

Drosophila SVMEMNRRMTTEQAKKTYERAIKMEQEFGEYFTGVVQGDITIEEYISKVKSMIWSQSGPTI 952
Human NIMEMNKRLTTEEQARKTFFERAMKLEQEFTEHFTAIVQGDLTLEDIYNQVKQIIIEEQSGSYI 918
.:*****:*****:***:***:*.******:***:*****:***:***:*.****.*

Drosophila WVPSKESL 960
Human WVPAKEKL 926
 :

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FIGURE 6C

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 2

BLASTP sequence alignment

Score = 621 bits (1601), Expect = e-176

Identities = 318/524 (60%), Positives = 390/524 (73%), Gaps = 43/524 (8%)



Query: 438 ESNQTNRRSQSPQRPQSGRYASTNVLAAPPPTPRAVSTEDITREPTITIQKGPQGLG 497 (SEQ ID NO:259)
+S T++ S RQP RAVS E EPR + + KG GLG

Sbjct: 389 DSEMTSHSQHSTATRQPSMTLQ-----RAVSLEG--EPRKVVHLHGKSTGLG 432 (SEQ ID NO:292)

Query: 498 FNIVGGEDGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGG 557

FNIVGGEDG+GI+VSFILAGGPADL EL+RGDQ+LSVN ++L A+HE+AA ALK +G

Sbjct: 433 FNIVGGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDLRGASHEQAAAALKGAGQ 492

Query: 558 VVTLAQYRPEEYNRFEARIQELKQQXXXXXXXXXXXXXXXXXX-QKRSLYVRALFDYDPNRD 616

VT++AQY+PE+Y RFEA+I +L++Q QKRSLYVRA+FDYD ++D

Query: 617 DGLPSRGLPFKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVPSKRRWERKMRARDS 676

Sbjct: 553 SGLPSQGLSFKYGDILHVINASDDEWWQARRVMLEGDSEEMGVIPSKRRVERKERARLKT 612

VKF ++ K S D++KK+F FSRKFPPF K++++ ++ SD E +

Sbjct: 613 VKFNAKPGVIDS--KGSFNDKRKKSFI FSRKFPFYKNKEQSEQETSDPE-----RGQE 663

Query: 737 DIXXXXXXXXXXXXXXXXXXVLSYEAVQRLSINYTRPVIIILGPLKDRINDDLISEYDPDKFG 796

D+ +LSYE V R INYTRPVIILGP+KDRINDDLISE+PDKFG

[illegible]

Query: 797 SCVPHTTRPKREYEVDGRDYHFVSSREQMERDIQNHLFIEAGQYNDNLYGTSVASVREVA 856

Sbjct: 707 SCVPHTTRPKRDYEVDGRDYHFVISREQMEKDIQEHKFIEAGQYNDNLYGTSVQSVRFVA 766

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

E+GKHCILDVSGNAIKRLQVAQLYP+A+FIKP+S++S+MEMN+R+TEEQAKKTY+RAIK+

Sbjct: 767 ERGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLESLMEMNKRLTEEQAKKTYDRAIKL 826

Query: 917 EQEFG EYFTGVVQGDTIEEIYSKVKS MIWSQSGPTIWVPSKESL 960

EQEFG EYFT +VQGDT+E+IY++ K +I QSGP IW+PSKE L

Sbjct: 827 EQEFGYFTAIVQGDTLEDIYNQCKLVIEEQSGPFIWIPSKEKL 870

Score = 197 bits (502), Expect = 7e-49

Identities = 111/221 (50%), Positives = 140/221 (63%), Gaps = 24/221 (10%)



Query: 23 SLFNLDVNGDD-SWLYEDIQLERGNGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAA 81 (SEQ ID NO:293)

+L + VNG + + +E+I LERGNSGLGFSIAGGTDNPHIG D I+ITK+I GGAAA

147304-19 122711-19012212122122122KONSOLOZ SINOCLIN MOBB ON KRAH SOHA 159

Query: 82 ADGRLXXXXXXXXXXXXXXXXXXXXPHASAVDALKKAGNVVKLHVKRKXXXXXXXXXXXXXXXXXXXX 141

DGRL H+ AV+ALK+AG++ +L+V+R+

Sbjct: 140 EDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARLYVRRRRPILET----- 190

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Query: 142 XXXXXXXXXXXXVIEIDLVKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLS 201
V+EI L KG KGLGFSIAGG+GNQHIPGDN IYVTK+ DGG AQ DGRL
Sbjct: 191 -----VVEIKLFKGPGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRQLQ 240

Query: 202 IGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIG 242
+GD+L+ V + +LE VTHE AVA LK+ ++ V L +G
Sbjct: 241 VGDRLLMV---NNYSLEEVTHEEAVAILKNTSEVVYLKVG 277
Score = 66.2 bits (160), Expect = 3e-09
Identities = 40/125 (32%), Positives = 64/125 (51%), Gaps = 11/125 (8%)



Query: 448 SPQPRQPGSRYASTNVLAAPPGTPRAVSTEDITREPTITIQKGPQGLGFNIVGGEDGQ 507 (SEQ ID NO:295)
SP P +T+ L +P V+ +I E IT+++G GLGF+I GG D
Sbjct: 65 SPLKASPAPIIVNTDTLDTIP-----YVNGTEIEYEFEEITLERGNSGLGFSIAGGTDNP 119 (SEQ ID NO:296)

Query: 508 -----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTL 561
GI+++ I+ GG A L+ D +L VN V+++ +H +A +ALK +G + L
Sbjct: 120 HIGDDPGIFITKIIPGAAAEDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARL 179

Query: 562 LAQYR 566
+ R
Sbjct: 180 YVRRR 184
Score = 65.5 bits (158), Expect = 5e-09
Identities = 38/81 (46%), Positives = 47/81 (57%), Gaps = 6/81 (7%)



Query: 487 ITIQKGPQGLGFNIVGGEDGQ-----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNL 540 (SEQ ID NO:297)
I + KGP+GLGF+I GG Q IYV+ I+ GG A L+ GD+LL VNN +L
Sbjct: 194 IKLFKGPGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRQLQVGDRLLMVNNYSL 253 (SEQ ID NO:298)

Query: 541 THATHEEAAQALKTSGGVVTL 561
THEEA LK + VV L
Sbjct: 254 EEVTHEEAVAILKNTSEVVYL 274
Score = 50.8 bits (120), Expect = 1e-04
Identities = 33/87 (37%), Positives = 48/87 (54%), Gaps = 10/87 (11%)



Query: 154 EIDLVKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNG 213 (SEQ ID NO:299)
++ L KG GLGF+I GG + GI+V+ + GG A + G L GD+++V NG
Sbjct: 421 KVV LHKGSTGLGFNIVGGEDGE-----GIFVSFILAGGPADLSGELQRGDQILSV--NG 472 (SEQ ID NO:300)

Query: 214 SEKNLENVTHELAVATLKSITDKVTLI 240
+ L +HE A A LK VT+I
Sbjct: 473 ID--LRGASHEQAAAALKGAGQTVTII 497
Score = 41.2 bits (95), Expect = 0.10
Identities = 24/81 (29%), Positives = 36/81 (43%), Gaps = 6/81 (7%)



Query: 41 IQLERGNISGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLXXXXXXXXXXXXX 100 (SEQ ID NO:301)
+ L +G++GLGF+I GG D I+++ ++GG A G L
Sbjct: 422 VVLHKGSTGLGFNIVGGEDG-----EGIFVSFILAGGPADLSGELQRGDQILSVNGIDL 475 (SEQ ID NO:302)

Query: 101 XXXPHASAVDALKKAGNVVKL 121
H A ALK AG V +
Sbjct: 476 RGASHEQAAAALKGAGQTVTI 496

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CLUSTAL W (1.82) sequence alignment

[illegible]

REPLACEMENT SHEET

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FIGURE 7

Hu-Dlg1	---MPVRKQDTQRALHLLEEYRSKLSQTEDRQLRSSIERVINIFQSNLFQ-ALIDIQEFY	56	(SEQ ID NO:267)
Hu-Dlg4	---MSQRPRAPRSALWLLAPPLLRWAPP-----LLTVLHSDLFQ-ALLDILDYY	45	(SEQ ID NO:304)
Hu-Dlg2	---MFFACYCALRTNVKKYRYQDEADPHDHS-----LPRLTHEVRGP-ELVHVSEK-	47	(SEQ ID NO:303)
Hu-Dlg3	MHKHQHCCKCPECYEVTRLAALRRLEPPGYG----DWQVPDPYGPGGGNGASAGYGGYS	55	(SEQ ID NO:305)
Dm-Dlg1	---MTTRKK-----KRDGG-----	11	(SEQ ID NO:259)
Hu-Dlg5	-----		(SEQ ID NO:306)

Hu-Dlg1	EVTLLDNPKCIDRSKPSEPIQPVNTWEISSLPSTVTSETLPSSLSPSVEKYRYQDETP	116
Hu-Dlg4	EASLSES-----QKYRYQDETP	63
Hu-Dlg2	NLSQIEN-----VHGYVLQSHISP	66
Hu-Dlg3	SQTLPSQAG-----ATPTPRTKAKLIP	77
Dm-Dlg1	-----	
Hu-Dlg5	-----	

Hu-Dlg1	PQEHISPQITNEVIGPELVHVSEKNLSEIENVHGFVSHSHISPIKPTAVLPSPPTVPVI	176
Hu-Dlg4	PLEHSP-----AHLPN-----	74
Hu-Dlg2	LK-----	68
Hu-Dlg3	TGRDVG-----PVPLKPVPGK-----	93
Dm-Dlg1	-----	
Hu-Dlg5	-----	

Hu-Dlg1	PVLPVPAENTVILPTIPQANPPVVLVNTDSLETP---TYVNGTDADYEYEEITLERGNSG	233
Hu-Dlg4	-----QANSPPVIVNTDTLEAPGYELQVNGTEGEMEYEEITLERGNSG	117
Hu-Dlg2	-----ASPAPIIVNTDTLDTIP---YVNGTEIEYEFEEITLERGNSG	107
Hu-Dlg3	-----STPKLNGSGPSWWPECTCTNRDWYEQVNGSDGMFKYEEIVLERGNSG	140
Dm-Dlg1	-----GSGGGFIKKVSSLFNLD---SVNGDD-SWLYEDIQLERGNSG	49
Hu-Dlg5	-----MRATHGSNSLPSSARLGSSSN	21

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Hu-Dlg1	LGFSIAGGTDNPHIGDDSSIFITKIITGGAAQDGRRLRVNDCILQVNEVDVRDVTHSKAV	293
Hu-Dlg4	LGFSIAGGTDNPHIGDDPSIFITKIIPGGAAQDGRRLRVNDSILFVNEVDVREVTHSAV	177
Hu-Dlg2	LGFSIAGGTDNPHIGDDPGIFITKIIPGGAAEDGRRLRVNDCILRVNEVDVSEVSHSKAV	167
Hu-Dlg3	LGFSIAGGIDNPHVPDDPGIFITKIIPGGAAAMDGRGLGVNDCVLRVNEVEVSEVSHSRV	200
Dm-Dlg1	LGFSIAGGTDNPHIGTDTSIYITKLISGGAAADGRSLINDIIVSVNDVSVVDVPHASV	109
Hu-Dlg5	LQFKAER-IKIPSTPRYPRSVVGSR--GSVSHSECSTPPQSPLNIDTLSSCSQSQTAS	78

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Hu-Dlg1	EALKEAGSIVRLYVKRRK-----PVS-----EKIMEIKLIKGPGLGFSI	333
Hu-Dlg4	EALKEAGSIVRLYVMRRK-----PPA-----EKVMEIKLIKGPGLGFSI	217
Hu-Dlg2	EALKEAGSIARLYVRRRR-----PIL-----ETVVEIKLFKGPGLGFSI	207
Hu-Dlg3	EALKEAGPVVRLVRRRQ-----PPP-----ETIMEVNLLKGPGLGFSI	240
Dm-Dlg1	DALKKAGNVVKLHVKKRK-GTATTPAAGSAAGDARDSAASGPKVIEIDLKGGKGLGFSI	168
Hu-Dlg5	TLPRIAVNPASLGERRKDR---PYV-----EPRHVVKVQKGEPLGISI	119

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Hu-Dlg1	AGGVGNQHIPGDNSIYVTKIIEGGAHKGDKLQIGDKLLAVNN---VCLEEVTHEEAVT	389
Hu-Dlg4	AGGVGNQHIPGDNSIYVTKIIEGGAHKGDKLQIGDKILAVNS---VGLEDVMHEDAVA	273
Hu-Dlg2	AGGVGNQHIPGDNSIYVTKIIDGGAAQDKGRLQVGDRLLMVNN---YSLEEVTHEEAVA	263
Hu-Dlg3	AGGIGNQHIPGDNSIYITKIIEGGAQDKGRLQIGDRLLAVNN---TNLQDVRHEEAVA	296
Dm-Dlg1	AGGIGNQHIPGDNGIYVTKLITDGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVA	228
Hu-Dlg5	VSGE-----KGGIYVSKVTVGSIAHQAG-LEYGDQLLEFNG---INLRSATEQQARL	167

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Hu-Dlg1	ALKNTSDFVYLKVAKPTSMYMDGYA-----	415
Hu-Dlg4	ALKNTYDVVYLKVAKPSNAYLSDSYA-----	299
Hu-Dlg2	ILKNTSEVVYLKVGNPPTIYMTDPYG-----	289
Hu-Dlg3	SLKNTSDMVYLKVAKPGSLHLNDMYA-----	322
Dm-Dlg1	TLKSITDKVTLLIIGKTQHLTTSASGGGGGLSSGQQLSQSQSLATSQSQSVHQQQHAT	288
Hu-Dlg5	IIGQQCDTITILAQYNPHVHQLSSHS-----	193

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Hu-Dlg1	-----	
Hu-Dlg4	-----	
Hu-Dlg2	-----	
Hu-Dlg3	-----	
Dm-Dlg1	PMVNSQSTGALNSMGQTVVDSPIPQAAAAVAAAANASASASVIASNNTISNTTVTTVTA	348

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Hu-Dlg5 -----

Hu-Dlg1 -----PP-----DITNSSSQPVDNHVS-----PSSFLG----- 438
Hu-Dlg4 -----PP-----DITTSYSQHLNEIS-----HSSYLGTD-----YP 326
Hu-Dlg2 -----PP-----DITHSYSPMENHLL-----SGNNGTLE-----YK 316
Hu-Dlg3 -----PP-----DYASTFTALADNHIS-----HNSSLGYLGAVESKVS 356
Dm-Dlg1 TATASNDSSKLPPSLGANSSISISNSNSNSNNINNINSINNNSSSSSTTATVAAATP 408
Hu-Dlg5 -----RSSSHLDPAAGTHSTLQ-----GSGTTTPEHPSVIDPLM 226
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Hu-Dlg1 --QTPASPARYSPPVSKAVLGDEITR----- 462
Hu-Dlg4 TAMTPTSPRRYSPVAKDLLGEEDIPR----- 352
Hu-Dlg2 TSLPPISPGRYSPIPKHMLVDDDYTRPPEPVYSTVNKLCDPASPRHYSPECDKSFLLS 376
Hu-Dlg3 PAPPQVPTRYSPPIPRHMLAEDFTR----- 382
Dm-Dlg1 TAASAAAAASSPPANSFYNNASMPALPVESNQTNNSQSPPQPGSRYASTN----- 462
Hu-Dlg5 EQDEGPSTPPAKQSSSRIAGDANKKT----- 252
.

Hu-Dlg1 -----EPRKVVLRHGSGTGLGFNIV 481
Hu-Dlg4 -----EPRRIVIHGSGTGLGFNIV 371
Hu-Dlg2 APYSHYHLGLLPDSEMTSHSQHSTATRQPSMTLQRAVSLEGEPRKVVLRHGSGTGLGFNIV 436
Hu-Dlg3 -----EPRKIILHKGSGTGLGFNIV 401
Dm-Dlg1 -----VLAAVPPGTPRAVSTEDITREPTITIQKGPQGLGFNIV 501
Hu-Dlg5 -----LEPRVVFIIKKSQLELGVHLC 272
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Hu-Dlg1 GGEDGEGIFISFILAGGPADLSGELRKGDRIISVNSVDLRAASHEQAAAAALKNAGQAVTI 541
Hu-Dlg4 GGEDGEGIFISFILAGGPADLSGELRKGDQILSVNGVDLRNASHEQAAIALKNAGQTVTI 431
Hu-Dlg2 GGEDGEGIFVSFILAGGPADLSGELRQGDQILSVNGIDLRGASHEQAAAAALKNAGQTVTI 496
Hu-Dlg3 GGEDGEGIFVSFILAGGPADLSGELRRGDRILSVNGVNLNRNATHEQAAAAALKNAGQSVTI 461
Dm-Dlg1 GGEDGQGIYVSFILAGGPADLSGELRKGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTL 561
Hu-Dlg5 GG-NLHGVPVAEVEDDSPAKGPDGLVPGDLILEYGS�DVRNKTVEEVYVEMLKPRDGVRL 331
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Hu-Dlg1 VAQYRPEEYSRFEAKIHDRLREQMNMSSISSGSGSLRTSQKRSLYVRALFDYDKTKDSGLP 601
Hu-Dlg4 IAQYKPEEYSRFEAKIHDRLREQMNMSSSLSGGTASLRSPKRGFYIRALFDYDKTKDCGFL 491
Hu-Dlg2 IAQYQPEDYARFEAKIHDRLREQMNMHSMSSGSGSLRTNQKRSLYVRAMFDYDKSKDSGLP 556
Hu-Dlg3 VAQYRPEEYSRFEAKIHDRLREQMNMSSSMSSGSGSLRTSEKRSLYVRALFDYDRTRDSCLP 521
Dm-Dlg1 LAQYRPEEYNRFEARIQELKQQAALGAGSGT-LLRTTQKRSLYVRALFDYDPNRDDGLP 620
Hu-Dlg5 KVQYRPEEFTKAG-----LPGDSFYIRALYDR-----LADV 363
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Hu-Dlg1 SQGLNFKFGDILHVINASDD---EWWQARQVTPDGESDEVGVIPSKRRVEKKERARLKT 658
Hu-Dlg4 SQALSFRFGDVLHVIDASDE---EWWQARRVHSDSETDDIGFIPSKRRVERREWSRLKAK 548
Hu-Dlg2 SQGLSFKYGDILHVINASDD---EWWQARRVMLEGDSEMGVIPSKRRVERKERARLKT 613
Hu-Dlg3 SQGLSFSYGDILHVINASDD---EWWQARLVTPHGESEQIGVIPSKRRVEKKERARLKT 578
Dm-Dlg1 SRGLPFFKHGDILHVTNASDD---EWWQARRVLGDNEDEQIGVIPSKRRWERKMRARDRSV 677
Hu-Dlg5 EQELSFKKDDILYVDDTLPOGTFGSWMWQLDENAQKIQRGQIPSKYVMDQEFSSRLSMS 423
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Hu-Dlg1 KFNSKT----RDKGQSFNDKRKNLFSRKFPFYKNKDQSEQETSDADQH----- 703
Hu-Dlg4 DWG----- 551
Hu-Dlg2 KFNAKPGVI--DSKGSFNDKRKKSFIFSRKFPFYKNKEQSE----- 654
Hu-Dlg3 KFHARTGMI--ESNRDFPGLSDDYY----- 601
Dm-Dlg1 KFQGHAAANNLQKQSTLDRKKKNFTFSRKFPFMKSREKNEGSDQEPNGVVSSTSEID 737
Hu-Dlg5 EVKDDNSATKTLASAAARRSFFRRKHKHKRSGSKDGKDLLALDAFS----- 468
.

Hu-Dlg1 VTSNASDSESSYRGQEEYVLSYEPVNVQEVNYTRPVIILGPMKDRINDDLISEFPDKFGS 763
Hu-Dlg4 -----SSSGSQGREDSVLSYETVTQMEVHYARPPIILGPTKDRANDDLISEFPDKFGS 604
Hu-Dlg2 -----TSDPERGQEDLILSYEPVTRQEIYNYTRPVIILGPMKDRINDDLISEFPDKFGS 707
Hu-Dlg3 -----GAKNLKGQEDAILSYEPVTRQEIHYARPVIILGPMKDRVNDLISEFPDKFGS 654
Dm-Dlg1 INNVMNNQSNQEPSEENVLSYEAQVRLSINYTRPVIILGPLKDRINDDLISEYDPDKFGS 797
Hu-Dlg5 -----SDSIPLFEDSVSLAYQRVQKVDCTALRPVLILGPLLDVVKEMLVNEAPGKFCR 521
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Hu-Dlg1 CVPHTTRPKRDYEVDRDYHFVTSREQMEKDIQEHKFIEAGQYNNHLYGTSVQSVREVAG 823
Hu-Dlg4 CVPHTTRPKREYIDGRDYHFVSSREKMEKDIQAHKFIEAGQYNSHLYGTSVQSVREVAE 664
Hu-Dlg2 CVPHTTRPKRDYEVDRDYHFVTSREQMEKDIQEHKFIEAGQYNDNLYGTSVQSVRVFAE 767
Hu-Dlg3 CVPHTTRPRDNEVDGQDYHFVVSREQMEKDIQDNKFIEAGQFNDNLYGTSIQSVRAVAE 714
Dm-Dlg1 CVPHTTRPKREYEVDRDYHFVSSREQMERDIQNHLEAGQYNDNLYGTSVSVASREVAE 857
Hu-Dlg5 CPLEVMK-----ASQQAIERGVKCLFVDYKRRSGHFDVTTVASIXEITE 566

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Hu-Dlg1	KGKHCILDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNK-----RLTEEQARKTFE	877
Hu-Dlg4	QGKHCIILDSANAVRRLQAALHHPAIAIFIRPRSLNVLEINK-----RITEEQARKAFD	718
Hu-Dlg2	RGKHCIILDSVGNAIKRLQVAQLYPIAIFIKPRSLSELMEMNK-----RLTEEQAKKTYD	821
Hu-Dlg3	RGKHCIILDSVGNAIKRLQQAQLYPIAIFIKPKSIEALMEMNR-----RQTYEQAKKIYD	768
Dm-Dlg1	KGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVSDVMEMNR-----RMTEEQAKKTYE	911
Hu-Dlg5	KNRHCLLDIAPHAIERLHHMHIYPIVIFIHYKSAKHIKEQRDP IYLRLDKVTQRHSKEQFE	626

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Hu-Dlg1      RAMKLEQEFTHEFTAIVQGDLTEDIYNQVKQIEEQQSGSYIWVPAKEKL 926
Hu-Dlg4      RATKLEQEFTCEFSAIVEGDSFEIYHKVRVIDLSGPYIWWPARERL 767
Hu-Dlg2      RAIKLEQEFGEYFTAIVQGDLTEDIYNQCKLVIEEQSGPFIWPSKEKL 870
Hu-Dlg3      KAMKLEQEFGEYFTAIVQGDSLSEIYNKIKQIEDQSGHYIWWSPPEKL 817
Dm-Dlg1      RAIKMEQEFGEYFTGVVQGDTEEIYSKVKSMIWSQSGPTIWWPSKESL 960
Hu-Dlg5      AAQKLEQESYRSYFTGTGIQGGLSSICTQILAMVNQEQNKVLWI PACPL- 674
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